Amendments to and Listing of the Claims:

Please cancel claims 20, 39, 43-45 and 48, ***and amend claims 38 and 40-42***, all without prejudice, as shown below in the following listing of all claims ever presented. The following listing of claims replaces all prior versions thereof.

1-29. **(Canceled)**

30. (Previously presented) A method for identifying a gene associated with a detectable phenotype in a fungus, comprising:

(a) transforming the fungus with a polynucleotide comprising a marker gene which would otherwise be transcriptionally active in the fungus but which has been inactivated by the insertion of a defective *Impala* transposon, said marker gene comprising, in the direction of transcription, a promoter regulatory sequence of the niaD gene from *Aspergillus nidulans* which is more than 0.4 kb long and which is functionally linked to the coding sequence of said marker gene;

(b) mobilizing the defective *Impala* transposon using a transposase, the expression of which is controlled, under conditions which allow the excision of the *Impala* transposon, and further controlling expression of the transposase so as to permit reinsertion and stabilization of the *Impala* transposon in the genome of the fungus;

(c) selecting at least one insertion mutant with said detectable phenotype; and

(d) isolating the gene into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (c).

31. (Previously presented) The method of claim 30, wherein the marker gene encodes an enzyme that is active in the fungus.

32. (Previously presented) The method of claim 31, wherein the marker gene

encodes a nitrate reductase or a nitrilase.

33. (Previously presented) The method of claim 32, wherein the marker gene is a nitrate reductase gene from *Aspergillus nidulans.*

34. (Previously presented) The method of claim 30, 31, 32, or 33, wherein *Impala* transposon is integrated into the promoter regulatory sequence.

35. (Previously presented) The method of claim 34, wherein the *Impala* transposon carries an additional marker gene.

36. (Previously presented) A method for identifying a gene associated with a detectable phenotype of interest in *Magnaporthe grisea,* comprising:

(a) transforming *Magnaporthe grisea* fungi which lack the detectable phenotype of interest with a polynucleotide comprising a selectable marker gene, the coding sequence of which is functionally linked to a promoter regulatory sequence which is functional in *Magnaporthe grisea,* wherein an inserted *Impala* transposon suppresses expression of the marker gene, to produce transformants;

(b) providing conditions which allow the transposition of the *Impala* transposon in the transformants;

(c) screening the transformants for the expression of the marker gene in order to select insertion mutants resulting from the transposition and re-insertion of the *Impala* transposon;

(d) selecting at least one insertion mutant with said detectable phenotype of interest; and

(e) isolating the gene into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (d).

37. (Previously presented) The method of claim 36, wherein the conditions which allow transpositions are provided include introducing a transposase.

38. **(Currently amended)** A method for identifying a gene associated with a detectable phenotype of interest in a fungus, comprising:

(a) transforming fungi which lack the detectable phenotype of interest with a polynucleotide comprising a selectable marker gene, the coding sequence of which is functionally linked to a promoter regulatory sequence which is functional in *Magnaporthe grisea,* wherein an inserted *Impala* transposon suppresses expression of the marker gene, to produce transformants;

(b) providing a transposase to allow the transposition of the *Impala* transposon in the transformants;

(c) screening the transformants for the expression of the marker gene in order to select insertion mutants resulting from the transposition and re-insertion of the *Impala* transposon;

(d) selecting at least one insertion mutant with said detectable phenotype of interest; and

(e) isolating the gene into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (d);

wherein the marker gene is selected from the group consisting of: (i) a reporter gene selected from the group consisting of glucuronidase and green fluorescent protein; (ii) a gene that confers tolerance to an antibiotic selected from the group consisting of hygromycin, phleomycin and sulfonylurea; and (iii) a gene that confers tolerance to a bialaphos herbicide.

39. **(Canceled)**

40. **(Currently amended)** The method of ~~claim 39~~ claim 38, wherein the marker gene is a reporter gene selected from the group consisting of glucuronidase and green

fluorescent protein.

41. **(Currently amended)** The method of ~~claim 39~~ claim 38, wherein the marker gene is a gene that confers tolerance to an antibiotic selected from the group consisting of hygromycin, phleomycin, and sulfonylurea.

42. **(Currently amended)** The method of ~~claim 39~~ claim 38, wherein the marker gene is the gene that confers tolerance to the herbicide bialaphos.

43-45. **(Canceled)**

46. **(Currently amended)** The method of claim 38, ~~39, or 43~~ wherein the *Impala* transposon is integrated into the promoter regulatory sequence.

47. **(Currently amended)** The method of claim 38, ~~39, or 43~~ wherein the *Impala* transposon is integrated into an intron of the marker gene.

48. **(Canceled)**

49. (Previously presented) A method for identifying a promoter of interest in a fungus, comprising:

(a) transforming fungi with a polynucleotide comprising a first marker gene, said first marker gene comprising a promoter regulatory sequence which is functional in *Magnaporthe grisea* functionally linked to the coding sequence of said first marker gene and an *Impala* transposon comprising a second marker gene, wherein expression of said first marker gene is inactivated by the insertion of the *Impala* transposon and the second marker gene lacks an operably linked promoter sequence, to produce transformants;

(b) providing conditions which allow the transposition of the *Impala*

transposon in the transformants;

(c) screening the transformants for the expression of the first marker select insertion mutants resulting from the transposition of the *Impala* element;

(d) selecting at least one insertion mutant which expresses the second marker gene; and

(e) isolating the promoter into which, or close to which, the *Impala* transposon has inserted in the insertion mutant selected in (d) to result in expression of the second marker gene.